

We claim:

1. A method of determining the clinical outcome of a subject with a cancer using a Genomic Damage Fraction comprising,

a. determining the relative change in quantity of nucleic acids between cancerous cells and non-cancerous cells of said subject;

b. determining the Genomic Damage Fraction from the results of step (a)

c. determining the prognosis of said subject according to said subject's GDF, where a GDF greater than a predetermined GDF is indicative of a first clinical outcome, and a GDF lesser than a predetermined GDF is indicative of a second clinical outcome.

2. The method of claim 1, wherein the relative change in quantity of nucleic acids is determined using AP-PCR DNA fingerprinting.

3. The method of claim 1, wherein said first clinical outcome is increased risk.

4. The method of claim 1, wherein said second clinical outcome is decreased risk.

5. The method of claim 1, wherein the relative change in nucleic acids is determined by the number of qualitative and/or quantitative changes in the DNA fingerprint bands present in the cancerous cells as compared with the normal cells.

6. The method of claim 5, wherein the relative change in nucleic acids is determined by the number of quantitative changes in the DNA fingerprint bands.

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c. generating the AP-PCR DNA fingerprint of metastatic cancer cells from said subject; and

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 d. identifying chromosomal regions from
 AP-PCR DNA fingerprint data of steps (a), (b) and (c)
 wherein the occurrence of gains or losses of nucleic
 acids in certain chromosomal regions is prognostic of the
 5 clinical outcome for said subject.

14. The method of claim 13, wherein the gain
 and loss of nucleic acids is significantly different in
 metastatic cancer cells as compared to primary cancer
 cells.

10 15. The method of claim 13, wherein said
 chromosomal region is determined by a band of
 chromosome 4 obtained using the Blue primer (SEQ ID
 No: 1).

15 16. The method of claim 15, wherein said band
 is band N from the DNA fingerprint generated with the
 Blue primer (SEQ ID. NO:1).

17. A method of determining the clinical
 outcome of a subject with a cancer comprising,

a. generating the AP-PCR DNA fingerprint of
 20 non-cancerous cells from said subject;

b. generating the AP-PCR DNA fingerprint of
 primary cancer cells from said subject;

c. identifying chromosomal regions from
 AP-PCR DNA fingerprint data of steps (a) and (b), where
 25 gains or losses of nucleic acids occur; and

d. comparing said AP-PCR DNA fingerprints of
 chromosomes 1, 4, 6, 8, 9, and 13 from step a and step b
 wherein presence of gain or loss of nucleic acids in
 certain chromosomal regions is prognostic of the clinical
 30 outcome for said subject.

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18. The method of claim 17 wherein said
 chromosomal region that is determined by band N of
 chromosome 4 from the BLUE primer (SEQ ID NO: 1)
 fingerprint is prognostic of the clinical outcome for
 5 said subject.

19. A method of predicting a clinical outcome
 of a subject with cancer using an amplotype from said
 subject comprising,

a. locating chromosomal regions that have
 10 gained and lost nucleic acids using AP-PCR DNA
 fingerprinting;

b. identifying said chromosomal regions that
 have lost nucleic acids; and

c. identifying said chromosomal regions that
 15 have gained nucleic acids;
 wherein the combination of gains and losses according to
 chromosomal regions are prognostic of the clinical
 outcome for subject with cancer.

20. The method of claim 19, wherein the
 20 results of step (b) and step (c) are displayed where said
 gains and losses of nucleic acids are listed according to
 the chromosomal regions where they occur, wherein the
 combination of gains and losses according to chromosomal
 regions are prognostic of the clinical outcome for
 25 subject with cancer.

21. A method of identifying a genomic region
 relevant for a cancer in a subject having said cancer
 comprising,

(a) generating the AP-PCR DNA fingerprint of
 30 non-cancerous cells, primary cancer, and metastatic tumor
 cells from said subject; and

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~~(b) identifying said genomic regions from AP-PCR DNA fingerprint data of step (a), showing gains and losses of nucleic acids in certain genomic regions thereby identifying a genomic region linked to a cancer gene.~~

~~22. The method of claim 21, wherein said cancer is colorectal cancer.~~

23. The method of claim 21, wherein the said AP-PCR DNA fingerprint is generated with the Blue primer
10 (SEQ ID NO: 1).

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